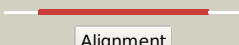



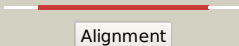
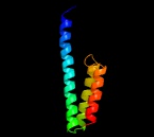
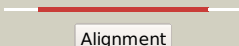


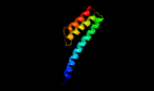
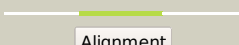

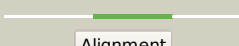
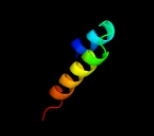
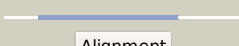
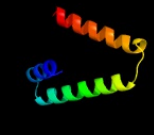
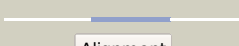




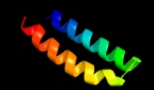


Phyre2

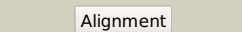
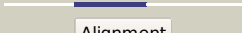




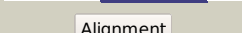
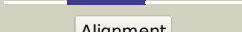


Email mdejesus@rockefeller.edu
 Description RVBD2412_(rpsT)_2710085_2710345
 Date Wed Aug 7 12:50:03 BST 2019
 Unique Job ID 67f9b08c895e44f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jt_	 Alignment		100.0	81	PDB header: ribosome Chain: T; PDB Molecule: 30s ribosomal protein s20; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	c5mmjt_	 Alignment		100.0	41	PDB header: ribosome Chain: T; PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
3	d2gy9t1	 Alignment		100.0	40	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
4	d2uubt1	 Alignment		100.0	35	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
5	c3bbnT_	 Alignment		100.0	31	PDB header: ribosome Chain: T; PDB Molecule: ribosomal protein s20; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
6	c5jnoB_	 Alignment		60.1	23	PDB header: cell cycle Chain: B; PDB Molecule: dna excision repair protein ercc-6-like; PDBTitle: crystal structure of the bd1-ntrp complex from bend3 and pich
7	c6a09C_	 Alignment		52.9	23	PDB header: unknown function Chain: C; PDB Molecule: yfdx protein; PDBTitle: salmonella typhi yfdx in the p222 space group
8	c5z1nA_	 Alignment		26.0	28	PDB header: protein binding Chain: A; PDB Molecule: g-protein interacting protein 1; PDBTitle: crystal structure of c terminal region of g-protein interacting2 protein 1 (gip1) from dictyostelium discoideum
9	c5tgyA_	 Alignment		21.8	37	PDB header: unknown function Chain: A; PDB Molecule: ps1; PDBTitle: nmr structure of holo-ps1
10	d2oo2a1	 Alignment		21.6	19	Fold: immunoglobulin/albumin-binding domain-like Superfamily: AF1782-like Family: AF1782-like
11	d1h6qa_	 Alignment		21.6	9	Fold: Mss4-like Superfamily: Mss4-like Family: Translationally controlled tumor protein TCTP (histamine-releasing factor)

12	c3dzaB_	Alignment		21.2	23	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized putative membrane protein; PDBTitle: crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
13	c5ig4A_	Alignment		20.4	13	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
14	d2k54a1	Alignment		19.9	23	Fold: Cystatin-like Superfamily: NTF2-like Family: Atu0742-like
15	d1txja_	Alignment		19.9	2	Fold: Mss4-like Superfamily: Mss4-like Family: Translationally controlled tumor protein TCTP (histamine-releasing factor)
16	c2oxoA_	Alignment		19.5	21	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
17	c3lysC_	Alignment		17.6	9	PDB header: recombination Chain: C: PDB Molecule: prophage pi2 protein 01, integrase; PDBTitle: crystal structure of the n-terminal domain of the prophage pi2 protein2 01 (integrase) from lactococcus lactis, northeast structural genomics3 consortium target kr124f
18	c2kj8A_	Alignment		17.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: putative prophage cps-53 integrase; PDBTitle: nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
19	c3k1sE_	Alignment		16.4	21	PDB header: transferase Chain: E: PDB Molecule: pts system, cellobiose-specific iia component; PDBTitle: crystal structure of the pts cellobiose specific enzyme iia from2 bacillus anthracis
20	c2dl1A_	Alignment		15.3	18	PDB header: protein transport Chain: A: PDB Molecule: spartin; PDBTitle: solution structure of the mit domain from human spartin
21	c2khvA_	Alignment	not modelled	15.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of protein nmu_a0922 from2 nitrospira multiformis. northeast structural genomics3 consortium target nmr38b.
22	c1xb2B_	Alignment	not modelled	14.9	25	PDB header: translation Chain: B: PDB Molecule: elongation factor ts, mitochondrial; PDBTitle: crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
23	d3en8a1	Alignment	not modelled	14.5	28	Fold: Cystatin-like Superfamily: NTF2-like Family: Rpa4348-like
24	d1yz1a1	Alignment	not modelled	14.1	5	Fold: Mss4-like Superfamily: Mss4-like Family: Translationally controlled tumor protein TCTP (histamine-releasing factor)
25	c5h1nB_	Alignment	not modelled	13.3	15	PDB header: unknown function Chain: B: PDB Molecule: upf0253 protein yaep; PDBTitle: crystal structure of sf173 from shigella flexneri
26	d1h7ca_	Alignment	not modelled	12.5	16	Fold: Spectrin repeat-like Superfamily: Tubulin chaperone cofactor A Family: Tubulin chaperone cofactor A
27	d2e2aa_	Alignment	not modelled	10.2	30	Fold: Spectrin repeat-like Superfamily: Enzyme Ila from lactose specific PTS, Ila-lac Family: Enzyme Ila from lactose specific PTS, Ila-lac
28	c5cxoA_	Alignment	not modelled	9.7	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: intriguing role of epoxide hydrolase/cyclase-like enzyme salbiii in2 pyran ring formation in polyether salinomycin

29	c3kspA_	Alignment	not modelled	9.0	21	PDB header: unknown function Chain: A: PDB Molecule: calcium/calmodulin-dependent kinase ii association domain; PDBTitle: crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
30	c2khqA_	Alignment	not modelled	9.0	20	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
31	c6j2yA_	Alignment	not modelled	8.6	16	PDB header: translation Chain: A: PDB Molecule: notctp; PDBTitle: solution structure of translationally controlled tumor protein from2 photosynthetic microalga nannochloropsis oceanica
32	c6of9G_	Alignment	not modelled	8.5	19	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
33	c3soyA_	Alignment	not modelled	8.4	13	PDB header: membrane protein Chain: A: PDB Molecule: ntf2-like superfamily protein; PDBTitle: nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
34	d1ohpa1	Alignment	not modelled	8.3	24	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
35	d1u00a1	Alignment	not modelled	8.3	13	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
36	d2a15a1	Alignment	not modelled	8.0	19	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
37	c2kj9A_	Alignment	not modelled	7.9	13	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
38	c4k12B_	Alignment	not modelled	7.3	16	PDB header: immune system/choline binding protein Chain: B: PDB Molecule: choline binding protein a; PDBTitle: structural basis for host specificity of factor h binding by2 streptococcus pneumoniae
39	c6h5IA_	Alignment	not modelled	7.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: similar to hydroxylamine oxidoreductase; PDBTitle: kueningenia stuttgartiensis reducing hao-like protein complex2 kustc0457/kustc0458
40	c4bgoA_	Alignment	not modelled	6.9	34	PDB header: hydrolase Chain: A: PDB Molecule: efem m75 peptidase; PDBTitle: structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
41	d2f86b1	Alignment	not modelled	6.9	20	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
42	c3l8rA_	Alignment	not modelled	6.7	23	PDB header: transferase Chain: A: PDB Molecule: putative pts system, cellobiose-specific iia PDBTitle: the crystal structure of ptca from s. mutans
43	c4adzA_	Alignment	not modelled	6.7	8	PDB header: transcription Chain: A: PDB Molecule: csor; PDBTitle: crystal structure of the apo form of a copper-sensitive operon2 regulator (csor) protein from streptomyces lividans
44	d3bb9a1	Alignment	not modelled	6.6	27	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
45	c4n4jA_	Alignment	not modelled	6.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxylamine oxidoreductase; PDBTitle: kueningenia stuttgartiensis hydroxylamine oxidoreductase
46	c2odmA_	Alignment	not modelled	6.3	17	PDB header: unknown function Chain: A: PDB Molecule: upf0358 protein mw0995; PDBTitle: crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
47	c3kh1B_	Alignment	not modelled	6.2	23	PDB header: hydrolase Chain: B: PDB Molecule: predicted metal-dependent phosphohydrolase; PDBTitle: crystal structure of predicted metal-dependent phosphohydrolase2 (zp_00055740.2) from magnetospirillum magnetotacticum ms-1 at 1.37 a3 resolution
48	d256ba_	Alignment	not modelled	6.1	14	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome b562
49	c5fmnB_	Alignment	not modelled	6.0	15	PDB header: dna binding protein Chain: B: PDB Molecule: inrs; PDBTitle: the nickel-responsive transcriptional regulator inrs
50	c4k7bA_	Alignment	not modelled	6.0	23	PDB header: photosynthesis Chain: A: PDB Molecule: extrinsic protein in photosystem ii; PDBTitle: crystal structure of extrinsic protein in photosystem ii
51	c3f14A_	Alignment	not modelled	6.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
52	c3zsuA_	Alignment	not modelled	6.0	12	PDB header: photosynthesis Chain: A: PDB Molecule: tl12057 protein; PDBTitle: structure of the cyanoq protein from thermosynechococcus elongatus

53	c1wcrA	 Alignment	not modelled	6.0	23	PDB header: transferase Chain: A: PDB Molecule: pts system, n, n'-diacetylchitobiose-specific PDBTitle: trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
54	c5x9jB	 Alignment	not modelled	6.0	19	PDB header: isomerase Chain: B: PDB Molecule: prhc; PDBTitle: structre of prhc from penicillium brasilianum nbrc 6234
55	c4u13B	 Alignment	not modelled	5.8	19	PDB header: transferase Chain: B: PDB Molecule: putative polyketide cyclase sma1630; PDBTitle: crystal structure of putative polyketide cyclase (protein sma1630)2 from sinorhizobium meliloti at 2.3 a resolution
56	c5ig5E	 Alignment	not modelled	5.7	10	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
57	d1aipc1	 Alignment	not modelled	5.6	39	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
58	d2ux0a1	 Alignment	not modelled	5.6	20	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
59	c2kkvA	 Alignment	not modelled	5.5	21	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of an integrase domain from protein spa42882 from salmonella enterica, northeast structural genomics consortium3 target slr105h
60	c3i0yC	 Alignment	not modelled	5.4	24	PDB header: isomerase Chain: C: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution
61	d2pv7a1	 Alignment	not modelled	5.1	9	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
62	c3aaiB	 Alignment	not modelled	5.0	10	PDB header: transcription Chain: B: PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8